SEQUENCE LISTING

<110> KLEIN, ROBERT
MATTHEWS, WILLIAM
MOORE, MARK
ALLEN, KEITH

<120> TRANSGENIC MICE CONTAINING TRP GENE DISRUPTION

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<141> 2000-10-26

<150> US 60/161,488
<151> 1999-10-26

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<170> PatentIn Ver. 2.0

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<223> Description of Artificial Sequence:primer

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tgtgctcctc tttggcttgc ttccaattaa ccctcactaa agggaacgaa t 51

<210> 22
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 22
ctggttcttg tctggcttgg cccaatgcaa caggtttcct gagcggtcat 50

<210> 23
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 23
ggtcctcgct ctgtgtccgt tgaacctcaa gctggcctac tatgcctat 49

<210> 24
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 24
tttgcgtgtc ctgtgtcgtc gaacgactaa atacgactca ctatagggcg 50

<210> 25
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 25
gccaatggac tcttagtttt ggaac 25

<210> 26
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 26
gttctggcaa acaaattcgg cgcac 25

<210> 27
<211> 51
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 27
tgtgctcctc tttggcttgc ttccaattaa ccctcactaa agggaacgaa t 51

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 28
ctggttcttg tctggcttgg cccaagttcc aaaactaaga gtccattggc 50

<210> 29
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 29
ggtcctcgct ctgtgtccgt tgaagtgcgc cgaatttgtt tgccagaac 49

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 30
gaaccttggt gtgccaagtt acttc 25

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 31
gaactttggc tgaacccctt gttct 25

<210> 32
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 32
tgtgctcctc tttggcttgc gttgaacgac taatacggac tcactatagg gcg 53

<210> 33
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 33
ctggttcttg tctggcttgg cccaagaagt aacttggcac accaaggttc 50

<210> 34
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 34
ggtcctcgct ctgtgtccgt tgaagaacaa ggggttcagc caaagttc 48

<210> 35
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 35
tttgcgtgtc ctgtgtcgtc gaattaaccc tcactaaagg gaacgaat 48

<210> 36
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 36
atgccggatc tcctactact gggcc 25

<210> 37
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 37
tgtcatagta gacagcgatg gaacg 25

<210> 38
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 38
gacaagaacc agttgacgtc aagcttcccg ggacgcgtgc tagcggcgcg ccg 53

<210> 39
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 39
ctggtcttgt ctggcttggc ccaaggccca gtagtaggag atccggcat 49

<210> 40
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 40
ggtcctcgct ctgtgtccgt tgaacgttcc atcgctgtct actatgaca 49

<210> 41
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
ctggttcttg tctggcttgg cccaaaaagc cgacagccac gctcacaagc 50

<210> 42
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 42
ggtcctcgct ctgtgtccgt tgaagcccaa tgccacagag agagaatgt 49

<210> 43

<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 43
ctggttcttg tctggcttgg cccaagttgg atcctctcca aggccccatc t 51

<210> 44
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
ggtcctcgct ctgtgtccgt tgaactccag tgccgagtgt gtggggacag 50

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 45
agctcagaca tggactccat ggccc 25

<210> 46
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 46
tgcgattgcc cagcaaatgc gaagt 25

<210> 47
<211> 1839
<212> DNA
<213> murine TRP

<400> 47
ggcacgaggg aggaagcgcc gccgggtccg ctctgctctg ggtccggctg ggccatggag 60
tccatgtctg agctcgcgcc ccgctgcctc ttatttcctt tgctgctgct gcttccgctg 120
ctgctccttc ctgccccgaa gctaggcccg agtcccgccg gggctgagga gaccgactgg 180
gtgcgattgc ccagcaaatg cgaagtgtgc aagtatgttg ctgtggagct gaagtcggct 240
tttgaggaaa cgggaaagac caaggaagtg attgacaccg gctatggcat cctggacggg 300
aagggctctg gagtcaagta caccaagtcg gacttacggt taattgaagt cactgagacc 360
atttgcaaga ggcttctgga ctacagcctg cacaaggaga ggactggcag caaccggttt 420
gccaagggta tgtcggagac ctttgagacg ctgcacaacc tagtccacaa aggggtcaag 480

gtggtgatgg atatccccta tgagctgtgg aacgagacct cagcagaggt ggctgacctc 540
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aaccaccagg aggaagacct gactgaattc ctctgtgcca accacgtgct gaagggaaag 660
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cagaggaagg aactgggggg cctgggggag gatgccaacg ccgaggagga ggagggtgtg 840
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atacagttcc ttctgttgtg gtgactccca cgcccccaca cacacaccat aaaattattt 1800
cgatgctgtt tcataactgt aaaaaaaaaa aaaaaaaaa 1839

<210> 48
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer with
cloning site

<400> 48
ctggttcttg tcggcttggc ccaaagctca gacatggact ccatggccc 49

<210> 49
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer with
cloning site

<400> 49
ggtcctcgct ctgtgtccgt tgaatgcgat tgcccagcaa atgcgaagt 49

<210> 50
<211> 471
<212> DNA
<213> homologue of T243

<220>
<221> modified_base
<222> (260)
<223> A, T, G or C

<400> 50
acagaaaaca agaaacaaaa accatgaaag atagtctgtt atccagggct agaatgccca 60
aggctggttc atccaaggta tgatgaaggt tcacccgcta ggaactgatg ctccagctac 120
tgagcctcct ttagctggca gtgatatcgc tatagggcgc caaagccacc atccgctctc 180
tgattgggtg agatgggaaa aaaaaaagat agttcctctc attggctata aagcagacgc 240
cgagcgaacc cattggttgn gtcgcccgcg ggccttggtc ggtttcgcaa gccgctagag 300
gctaccgggc gaggggcggg ccggagctcg ccgttgccgt ggttacccag agacacgtgc 360
gcagtcccgg aagcggccgg gggaagctgc tccgcgcgcg ctgccggagg aagcgccgcc 420
gggtccgctc tgctctgggt ccggctgggc catggagtcc atgtctgagc t 471

<210> 51
<211> 370
<212> DNA
<213> homologue of T243

<400> 51
tgcgattgcc cagcaaatgc gaaggtgagg gggcggggcc gcggggcgta gccaagcccg 60
aggggcggga gggggcgggg cctgtgggaa gggtctgggc ctggcaggac ctgggctggg 120
gtctccttgg ccctgctgtg tgctttgcgg caatgctggg tgctgtgact ctcggataac 180
ctggagatcc ctgcttttgg gcgaatccgg gggtagttgc tcatcaagac tagaggtggg 240
ggtggaggga aggcttcata caggaagcct gctgcgaaat gaagagttgg ccagggaaag 300
catggcgtgc agaggaactc actccgcaga aaccacagaa acagaggcag atgaggacgc 360
cctgccggcc 370

<210> 52
<211> 276
<212> PRT
<213> murine TRP

<400> 52
Met Glu Ser Met Ser Glu Leu Ala Pro Arg Cys Leu Leu Phe Pro Leu
1 5 10 15

Leu Leu Leu Leu Pro Leu Leu Leu Leu Pro Ala Pro Lys Leu Gly Pro
20 25 30

Ser Pro Ala Gly Ala Glu Glu Thr Asp Trp Val Arg Leu Pro Ser Lys
35 40 45

Cys Glu Val Cys Lys Tyr Val Ala Val Glu Leu Lys Ser Ala Phe Glu
50 55 60

Glu Thr Gly Lys Thr Lys Glu Val Ile Asp Thr Gly Tyr Gly Ile Leu
65 70 75 80

Asp Gly Lys Gly Ser Gly Val Lys Tyr Thr Lys Ser Asp Leu Arg Leu
85 90 95

Ile Glu Val Thr Glu Thr Ile Cys Lys Arg Leu Leu Asp Tyr Ser Leu
100 105 110

His Lys Glu Arg Thr Gly Ser Asn Arg Phe Ala Lys Gly Met Ser Glu
115 120 125

Thr Phe Glu Thr Leu His Asn Leu Val His Lys Gly Val Lys Val Val
130 135 140

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Met Asp Ile Pro Tyr Glu Leu Trp Asn Glu Thr Ser Ala Glu Val Ala
145                 150                 155                 160

Asp Leu Lys Lys Gln Cys Asp Val Leu Val Glu Glu Phe Glu Glu Val
                165                 170                 175

Ile Glu Asp Trp Tyr Arg Asn His Gln Glu Glu Asp Leu Thr Glu Phe
            180                 185                 190

Leu Cys Ala Asn His Val Leu Lys Gly Lys Asp Thr Ser Cys Leu Ala
        195                 200                 205

Glu Arg Trp Ser Gly Lys Lys Gly Asp Ile Ala Ser Leu Gly Gly Lys
    210                 215                 220

Lys Ser Lys Lys Lys Arg Ser Gly Val Lys Gly Ser Ser Ser Gly Ser
225                 230                 235                 240

Ser Lys Gln Arg Lys Glu Leu Gly Gly Leu Gly Glu Asp Ala Asn Ala
                245                 250                 255

Glu Glu Glu Glu Gly Val Gln Lys Ala Ser Pro Leu Pro His Ser Pro
            260                 265                 270

Pro Asp Glu Leu
        275
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<210> 53
<211> 1848
<212> DNA
<213> expanded T243

<400> 53

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ggcacgaggg aggaagcgcc gccgggtccg ctctgctctg ggtccggctg ggccatggag 60
tccatgtctg agctgctgct gctgctgctg ctgctgctgc tgctgctgct gctgctgctg 120
ctgctgctgc tgctgctgct gctgctgctg ctgctgctgc tgctgctgct gctgctgctg 180
ctgctgctgc tgcgattgcc cagcaaatgc gaagtgtgca agtatgttgc tgtggagctg 240
aagtcggctt ttgaggaaac gggaaagacc aaggaagtga ttgacaccgg ctatggcatc 300
ctggacggga agggctctgg agtcaagtac accaagtcgg acttacggtt aattgaagtc 360
actgagacca tttgcaagag gcttctggac tacagcctgc acaaggagag gactggcagc 420
aaccggtttg ccaagggtat gtcggagacc tttgagacgc tgcacaacct agtccacaaa 480
ggggtcaagg tggtgatgga tatcccctat gagctgtgga acgagacctc agcagaggtg 540
gctgacctca agaagcagtg tgacgtgctg gtggaagagt ttgaagaggt gattgaggac 600
tggtacagga accaccagga ggaagacctg actgaattcc tctgtgccaa ccacgtgctg 660
aagggaaagg acacgagttg cctagcagag cggtggtctg gcaagaaggg ggacatagcc 720
tccctgggag ggaagaaatc caagaagaag cgcagcggag tcaagggctc ctccagtggc 780
agcagcaagc agaggaagga actgggggc ctgggggagg atgccaacgc cgaggaggag 840
gagggtgtgc agaaggcatc gcccctccca cacagccccc ctgatgagct gtgagcccag 900
cttagtgtcc ttgaatcaag acccctgact tcagagcttg ggacacgcac agcgcagcgc 960
agcgcagctc cagcaaggac agctgctgtc cagcatcagg tctcctccct tggctgtgcc 1020
cctttccttc ccttgaacaa cagcaagagg tggaaggatc tggggtgctg ggagacggca 1080
ccccaaaggg aagaggagga ggagcagaag gcagctctct ttctacacag tccccctcac 1140
gagctccggg gtccacccag catccccagg ctgagatcca ggctcctgac atggaagctg 1200
aagagcatga ggcacataag atgctcacca gcgccccctt cagccaggaa ggactccgtg 1260
cagcctcagc agccaggcct gcctcttcct tccaccaagc attctcttct gctggtcctt 1320
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gtcggatggt aaattcgaga acttccagga caaactcggg tgtggcacaa aggggctgga 1380
cgccagagcc agagccacgc cagagactgc agagagggca cctgacctaa ccccccctgga 1440
aagccaatct gcagttcccg tgtccaccca ctcctcctga ggacgcctca tgctctgccc 1500
agcccttctc ccagggctac cagagtaaac acctttggc ctttcggttt ggttcctggg 1560
tcctcatcag cctccagagt gtcccctcat cgatcttttt tgcctttgtc ccccaatccc 1620
aggggctgga aggccatcac catcattgga ggcttaacct gtcagttact aggaggtgct 1680
gggagcgccc ggggttggtt tggggtaatc actcactggc tctcagcctt ctaacactgc 1740
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aaattatttc gatgctgttt cataactgta aaaaaaaaaa aaaaaaaa 1848

<210> 54
<211> 279
<212> PRT
<213> expanded T243

<400> 54
Met Glu Ser Met Ser Glu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu
20 25 30

Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg Leu
35 40 45

Pro Ser Lys Cys Glu Val Cys Lys Tyr Val Ala Val Glu Leu Lys Ser
50 55 60

Ala Phe Glu Glu Thr Gly Lys Thr Lys Glu Val Ile Asp Thr Gly Tyr
65 70 75 80

Gly Ile Leu Asp Gly Lys Gly Ser Gly Val Lys Tyr Thr Lys Ser Asp
85 90 95

Leu Arg Leu Ile Glu Val Thr Glu Thr Ile Cys Lys Arg Leu Leu Asp
100 105 110

Tyr Ser Leu His Lys Glu Arg Thr Gly Ser Asn Arg Phe Ala Lys Gly
115 120 125

Met Ser Glu Thr Phe Glu Thr Leu His Asn Leu Val His Lys Gly Val
130 135 140

Lys Val Val Met Asp Ile Pro Tyr Glu Leu Trp Asn Glu Thr Ser Ala
145 150 155 160

Glu Val Ala Asp Leu Lys Lys Gln Cys Asp Val Leu Val Glu Glu Phe
165 170 175

Glu Glu Val Ile Glu Asp Trp Tyr Arg Asn His Gln Glu Glu Asp Leu
180 185 190

Thr Glu Phe Leu Cys Ala Asn His Val Leu Lys Gly Lys Asp Thr Ser
195 200 205

Cys Leu Ala Glu Arg Trp Ser Gly Lys Lys Gly Asp Ile Ala Ser Leu
210 215 220

Gly Gly Lys Lys Ser Lys Lys Lys Arg Ser Gly Val Lys Gly Ser Ser
225 230 235 240

Ser Gly Ser Ser Lys Gln Arg Lys Glu Leu Gly Gly Leu Gly Glu Asp
245 250 255

Ala Asn Ala Glu Glu Glu Glu Gly Val Gln Lys Ala Ser Pro Leu Pro
260 265 270

His Ser Pro Pro Asp Glu Leu
275

<210> 55
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 55
gggccatgga gtccatgtct gagct 25

<210> 56
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
acttcgcatt tgctgggcaa tcgca 25

<210> 57
<211> 1362
<212> DNA
<213> human TRP

<400> 57
cgagccatgg attcaatgcc tgagcccgcg tcccgctgtc ttctgcttct tcccttgctg 60
ctgctgctgc tgctgctgct gccggccccg gagctgggcc cgagccaggc cggagctgag 120
gagaacgact gggttcgcct gcccagcaaa tgcgaagtgt gtaaatatgt tgctgtggag 180
ctgaagtcag cctttgagga aaccggcaag accaaggagg tgattggcac gggctatggc 240
atcctggacc agaaggcctc tggagtcaaa tacaccaagt cggacttgcg gttaatcgaa 300
gtcactgaga ccatttgcaa gaggctcctg gattatagcc tgcacaagga gaggaccggc 360
agcaatcgat ttgccaaggg catgtcagag acctttgaga cattacacaa cctggtacac 420
aaaggggtca aggtggtgat ggacatcccc tatgagctgt ggaacgagac ttctgcagag 480
gtggctgacc tcaagaagca gtgtgatgtg ctggtggaag agtttgagga ggtgatcgag 540
gactggtaca ggaaccacca ggaggaagac ctgactgaat tcctctgcgc caaccacgtg 600
ctgaagggaa aagacaccag ttgcctggca gagcagtggt ccggcaagaa gggagacaca 660
gctgccctgg gagggaagaa gtccaagaag aagagcagca gggccaaggc agcaggcggc 720
aggagtagca gcagcaaaca aaggaaggag ctgggtggcc ttgagggaga ccccagcccc 780
gaggaggatg agggcatcca gaaggcatcc cctctcacac acagcccccc tgatgagctc 840
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catggctctg gcaggccggg atggccccgc agccttcagc ccctccttgc cttggctgtg 960
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agggtactag gactgcagcc ccctgtagct cctctctgct taccctcct gtggacacct 1260
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1362

<210> 58
<211> 278
<212> PRT
<213> human TRP

<400> 58
Met Asp Ser Met Pro Glu Pro Ala Ser Arg Cys Leu Leu Leu Leu Pro
1 5 10 15

Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro Ala Pro Glu Leu Gly Pro
20 25 30

Ser Gln Ala Gly Ala Glu Glu Asn Asp Trp Val Arg Leu Pro Ser Lys
35 40 45

Cys Glu Val Cys Lys Tyr Val Ala Val Glu Leu Lys Ser Ala Phe Glu
50 55 60

Glu Thr Gly Lys Thr Lys Glu Val Ile Gly Thr Gly Tyr Gly Ile Leu
65 70 75 80

Asp Gln Lys Ala Ser Gly Val Lys Tyr Thr Lys Ser Asp Leu Arg Leu
85 90 95

Ile Glu Val Thr Glu Thr Ile Cys Lys Arg Leu Leu Asp Tyr Ser Leu
100 105 110

His Lys Glu Arg Thr Gly Ser Asn Arg Phe Ala Lys Gly Met Ser Glu
115 120 125

Thr Phe Glu Thr Leu His Asn Leu Val His Lys Gly Val Lys Val Val
130 135 140

Met Asp Ile Pro Tyr Glu Leu Trp Asn Glu Thr Ser Ala Glu Val Ala
145 150 155 160

Asp Leu Lys Lys Gln Cys Asp Val Leu Val Glu Glu Phe Glu Glu Val
165 170 175

Ile Glu Asp Trp Tyr Arg Asn His Gln Glu Glu Asp Leu Thr Glu Phe
180 185 190

Leu Cys Ala Asn His Val Leu Lys Gly Lys Asp Thr Ser Cys Leu Ala
195 200 205

Glu Gln Trp Ser Gly Lys Lys Gly Asp Thr Ala Ala Leu Gly Gly Lys
210 215 220

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Lys Ser Lys Lys Lys Ser Ser Arg Ala Lys Ala Ala Gly Gly Arg Ser
225                 230                 235                 240

Ser Ser Ser Lys Gln Arg Lys Glu Leu Gly Gly Leu Glu Gly Asp Pro
                245                 250                 255

Ser Pro Glu Glu Asp Glu Gly Ile Gln Lys Ala Ser Pro Leu Thr His
            260                 265                 270

Ser Pro Pro Asp Glu Leu
        275


<210> 59
<211> 107
<212> DNA
<213> deletion generated by knockout

<400> 59
cgcgccccgc tgcctcttat ttcctttgct gctgctgctt ccgctgctgc tccttcctgc 60
cccgaagcta ggcccgagtc ccgccggggc tgaggagacc gactggg               107
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